

1 AAGCTTCGCG GCCTCTGCAG AKGACTTGTG CAAACACTTC CTCTCTGGAC
51 AAGGAGGAAT GCAGGAGGCC ACCGCCTGCA GTACATCTTG GAGTGTGGA
101 GGGATGTGCC TGCACTTGTG AACGGGCGCC AGGAGAATGA GGCCCCAACC
151 AAGCCCGGCA GTGCCCAGTA GATGCAGAGA GGCACCCGTG CCCCAGTGA
201 GGGCACAGCC AGTGGGCATC CCTGAGGCCC AGGGGCCCCGT TCCTCTCCAC
251 TCCCAACAGA TCGCTCTGCT GTGGGGCCCT GGGAGGCCCT TCCTCGCCCT
301 GCTTCTGCTG GTTCCATCA AGCAAGTTAC AGGATCGCTC CTCAAGGAGA
351 CAACTCAGAA GTGGGCTAAT TATAAGGAGA AGTGTCTGGA AGACTTGCAC
401 AATAGACTTT CTGGCATATT TTGTAATGGG ACATTTGATC GGTATGTGTG
451 CTGGCCCTCAT TCTTATCTTG GAAATGTCTC TGTTCCTGT CTTTCATACT
501 TACCTTGGTG GAATGCAGAG AGCCCAGGAA GGGCCTACAG ACACTGCTTG
551 GCTCAGGGGA CTTGGCAGAC GCGAGAGAAC ACCACAGATA TTTGGCAGGA
601 TGAATCAGAA TGCTCAGAGA ACCACAGCTT CAGACAAAAC GTGGATCACT
651 ACGCCTTGCT ATACACCTTG CAGCTGATGT ACACTGTGGG CTACTCCGTG
701 TCTCTCATCT CCCTCTTCTT GGCTCTTACA CTCTTCTGT TCCTTCGAAA
751 ACTGCATTGC ACACGCAATT ACATCCACAT GAACCTGTTT GCTTCGTTCA
801 TCCTGAAAGT TCTGGCTGTC CTGGTGAAGG ACATGGTCTC CCACAACTCT
851 TACTCCAAGA GGCCCGATGA TGAGAGTGA TGGATGTCT ATCTGTCAGA
901 GACATCCGTC TCCTGTGCT CCGTCCAGGT CCTCCTGCAC TACTTTGTGG
951 GCACCAATCA CTTGTGGCTG CTGGTTGAAG GACTTTACCT CCACACTCTG
1001 CTGGAGCCCA CAGTGTITCC TGAAAGGCGG CTGTGGCCCA AGTACCTGGT
1051 GGTGGGTGG GCCTTCCCCA TGCTGTTTGT TATTCCCTGG GGTITGCCC
1101 GTGCACACCT GGAGAACACA CGGTGCTGGG CCACAAATGG GAACCTGAAA
1151 ATCTGGTGA TCATCAGAGG ACCCATGCTG CTTTGTGTAA CAGTTAATT
1201 CTTTCATCTC CTCAAGATTC TCAAGCTTCT CATTTCTAAG CTCAAAGCTC
1251 ATCAGATGTG CTTCAAGAGAC TACAAATACA GATTGGCGAA ATCAAAGTTG
1301 CTCCTCATTC CTTTGTGGG GGTTCATGAG GTCCTCTTCA CTTTCTCCC
1351 CGACGACCAA GTTCAAGGAT TTTCAAACG TATTCGACTC TTCATCCAGC
1401 TGACACTGAG CTCTGTCCAC GGATTTCTGG TGGCCTTGCA GTATGGCTTT

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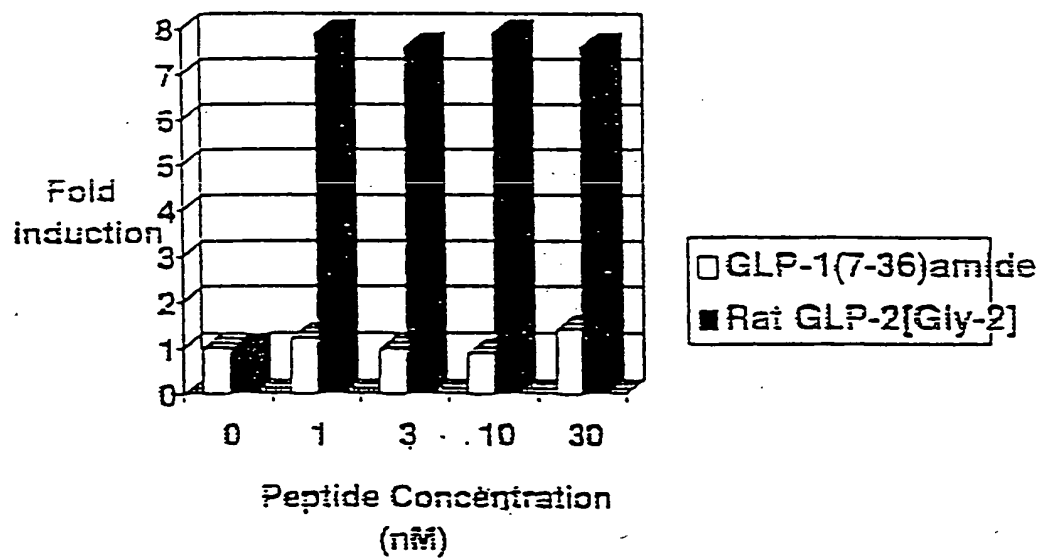
1451 GCCAATGGAG AGGTGAAGGC AGAGCTGCGA AAGTCATGGG GCCGCTTCTT
1501 ATTAGCCCCG CACTGGGGCT GCAGAACCTG TGTCTGGGG AAGAATTTC
1551 GGTTCCTGGG GAAGTGTTC AAGAAGCTGT CGGAGGGAGA TGGCTCTGAG
1601 AACTCCAGA AGCTGCGGT CTCCACATGC AGCTCACACC TGGCTCTGA
1651 GACCCTGGGA GACGTGGGG TACAGCCTCA CAGGGGCCGT GGAGCTTGGC
1701 CCCGGGGAAG CAGCCTGTCT GAGAGCAGTG AGGGAGACTT CACCCTGGCC
1751 AATACGATGG AGGAGATTCT GGAAGAGAGT GAGATCTAAG GCAGGGTCCA
1801 TCACCGCAGC TTGGCCACTG ARGAmCCAAC CcTARGAAGG ATKTTGCCGA
1851 RCCCARGGTC CTCCTCTTCC TATGTWctAT MCCCATTITG ATGTGAAGTC
1901 TCTCCTGGGT GAMCAASCTC TGTACCAACS ARTCTCagTC CCTCTTGCCC
1951 TTGTCAcCCT ACTACCCCTC CCCCATCaCa CATgTTTTCC AGAATKTCGG
2001 TTGTTTGGG GGGGGGGTc TTGCCCTAAA TTCAAGTsGA GTGGARCCCA
2051 CCATGAAGAA AARTCATTTA TTAAATAGAR TCCGGTTAGG ATCTCCTTCC
2101 CGTTCATGGT GCATGGCCTC CTTCCAAGGG ATGGGAGTCG GSTGCACTGG
2151 AACCCACAG GAAAcTTGA AGTATCCAGT TCTAGGGAAT TATAGCCAAT
2201 ATTCTGAGAG AGCAAGTCTG AGATGAGAKC CGAGAATWGC AAGTGTWGA
2251 CAWGCAITCA AGGAACTCC TCACCTTTgG GCGAAACCTA tGGCAGGATc
2301 GGCAtGGAGC AGCTATTMTG CAAYGGCCGC TCACCTGGGA CATACCACTC
2351 TCCTTGGGCA GGATGTGACC CCATGTKGTC CCCCAGACTC CTCTCCTCCT
2401 TGCTTSTSTT CYTTTCCYGT CAAGTCTCAC CTCCCTTTCT ACATCTCAGT
2451 TCWGTTTGGT GTYGACAGAA GYTTGAATGT CACAATACTG CATGTGTTAG
2501 TTTCTGTCGT CATTGCTGTG TCCAAATACC TGACCAGGAC CAATTTAAGC
2551 GAGGAACTGC TACATGGGCG GCCGC

FIGURE 1

1 MRPQSPAVP SRCREAPVPR VRAQPVGIPE AQGPVPLHSQ QMRLWGPGR
51 PFLALLLLVS IKQVTGSLK ETTQKWANYK EKCLEDLHNR LSGIFCNGTF
101 DRYVCWPHSY PGNVSVPCPS YLPWWNAESP GRAYRHCLAQ GTWQTRENTT
151 DIWQDESECS ENHSFRQNV D HYALLYTLQL MYTVGYSVSL ISLFLALTLF
201 LFLRKLHCTR NYIHMNLFAS FILKVLAVLV KDMVSHNSYS KRPDES GWM
251 SYLSETSVSC RSVQVLLHYF VGTNHLWLLV EGLYLHTLLE PTVFPERRLN
301 PKYLVVGWAF PMLFVIPWGF ARAHLENTRC WATNGNLKIW WIIRGPMLLC
351 VTVNFFIFLK ILKLLISKLK AHQMCFRDYK YRLAKSTLLL IPLLGVEVL
401 FTFFPDDQVQ GFSKRIRLFI QLTLSVHGF LVALQYG FAN GEVKAELRKS
451 WGRFILLARHW GCRTCVLGKN FRFLGKCSKK LSEG DGSETL QKLRFTCSS
501 HLASETLGDV GVQPHRGRCA WPRGSSLSES SEGDFTLANT MEEILEESEI

FIGURE 2

Figure 3

cAMP Response of COS Transfected with Clone

HGLP2 Human GLP-2 Receptor C4-4 vs C9-2R PCR from Clone HHT13

```

1  TCTTCTCTCTC TATCTCCCT GTTCTTGGCT CTCACCTTCC TCTTGTTCCT
51  TCGAAACTCTC CACTGCAAGC GCAACTACAT CCACATGAACT TTGTTTGCTT
101 CTTTCATCTCT GAGAACCTTG GCTGTACTTG TGAAGGACGT CGTCTTCTAC
151 AACTCTTACTC CCAGAGGGCC TGACATGAG AATGGGTGGA TGTCTTACCT
201 GTCAGAGATG TCCACCTCCT GCCGCTCAGT CCAGGTTCTC TTGCATTACT
251 TTGTGGGTGC CAATTACTTA TGGCTGCTGG TTGAAGGCTT CTACCTCCAC
301 ACGCTGCTGG AGCCCACTGT GCTTCTGTAG AGGCGGCTGT GGCCCAATA
351 CCTGCTCTTG GGTGSGGCT TCCCTGTGCT ATTTGTTGTA CCGTGGGGTT
401 TCGCCCTGTC ACACCTGGAR AACACAGGCT GCTGGACAAC AATGGGAAT
451 AAGAAATCTC GGTGGATCAT CCGAGGACCC ATGATGCTCT GTTAACAGT
501 CAATTCTCTC ATCTTCTGA AATTCTCAA GCTTCTCATT TCTAAGCTCA
551 AAGCTCATCA AATGTGCTTC AGAGATTATA AATACAGATT GGCAAAATCA
601 ACACTGGTCC TCATTCTTTT ATTGGGCTTT CATGAGATCC TCTTCTCTTT
651 CACTACTGAT GATCAAG

```

Figure 4

S F S L I S L F L A L T L L L F L R K L
 TCCTTCTCTCTTATCTCCCTCTTCCCTGCTCTCAGCTCTCTCTTCTCTTCTCGAATCTC
 1 ----- 61

H C T R N Y I H M N L F A S F I L R T L
 CACTGCACGGCGCAACTACATCCACATGAAGTTGTTTGTCTCTTCTCTCTGAGAACCTG
 61 ----- 120

A V L V K D V V F Y N S Y S K R P D N E
 GCTGTACTGGTGAAGGACCTCGTCTTCTACAACTCTTACTCCAAGAGGCTGACAAATGAG
 121 ----- 180

N G W M S Y L S E M S T S C R S V Q V L
 AATGGGTGGATGTCCTACCTGTCCAGAGATGTCCACCTCTCTGCTCTCACTCCAGGTTCTC
 181 ----- 240

L R Y F V G A N Y L W L L V E G L Y L H
 TTGCATTACTTTGTGGGTGCCAATTACTTATGCTGCTGGTTGAAGGCTCTACCTCCAC
 241 ----- 300

T L L E P T V L P E R R L W P K Y L L L
 ACCCTGCTGGAGCCCCACAGTGTCTCTGAGAGGGGCTGTGGCCCAATACCTGCTGTG
 301 ----- 360

G W A F P V L F V V P W G F A R A H L E
 GGTGGGGCTTCCCTGTCTATTTGTGTACCTGGGCTTTCCCTGCTGACACCTGGAR
 361 ----- 420

N T G C W T T N G N K K I W W I I R G P
 AACACAGGGTCTCTGGACAAACAAATGGGAATAAGAAATCTGCTGGATCATCCGAGGACCC
 421 ----- 480

M N L C V T V N F F I F L K I L K L L I
 ATGATGCTCTGTGTACAGTCAATTTCTTCATCTCTCTGAAAATCTCAAGCTTCTCAT
 481 ----- 540

S K L K A H Q M C F R D Y K Y R L A K S
 TCTAAGCTCAAAGCTCATCAATGTGCTTCAGAGATTATAAATACAGATTGGCAAAATCA
 541 ----- 600

T L V L I P L L G V H E I L F S F I T D
 ACACTGGTCTCTATTCCTTTATTGGGCTTCTAGAGATCTCTCTCTCTTCATCACTGAT
 601 ----- 660

D Q
 GATCAAG
 661 ----- 667

Figure 5

(SEQ ID NO: 11)

1 TGGAGAGGATTGTGCAAAACATTTCTTCTGTGGACCAAGAGGAATGCAAGAGGAGGCTGC 50
 61 CTGCGGTGCATCTTGGACGGCTAGAGAGATGTACCCCTACTTGTGAAGGTGCACGAGGAA 120
 121 M K L G S S R A G P G R G S A G L L P G 130
 GATGAAGCTGGGATCGAGCAGGGCAGGGCCTGGGAGAGGAAGCGCGGGACTCCTGCCTGG
 181 V E E L P M G I P A P W G T S P L S F H 240
 CGTCCACGAGCTGCCCATGGGCATCCCTGCCCCCTGGGGGACCAGTCTCTCTCCTTCCA
 241 R K C S L W A P G R P F L T L V L V S 300
 CAGGAAGTGCTCTCTCTGGGCCCCCTGGGAGGCCCTTCTCACTCTGGTCTCTGGTTTC
 301 I K Q V T G S L L E E T T R K W A Q Y K 350
 CATCAAGCAAGTTACAGGATCCCTCCTTGAGGAACGACTCGGAAGTGGGCTCAGTACAA
 361 Q A C L R D L L K E P S G I F C N G T F 420
 ACAGGCATGTCTGAGAGACTTACTCAAGGAACCTTCTGGCATATTTTGTAACGGGACATT
 421 D Q Y V C W P H S S P G N V S V P C P S 430
 TGATCAGTACGTGTGTGGCCTCATTTCTCTCTGGAAATGTCTCTGTACCCTGCCCTTC
 481 Y L P W W S E E S S G R A Y R H C L A Q 540
 ATACTTACCTTGGTGGAGTGAAGAGAGCTCAGGAAGGGCCTACAGACACTGCTTGGCTCA
 541 G T W Q T I E N A T D I W Q D D S E C S 600
 GGGGACTTGGCAGACGATAGAGAACGCCACGGATATTGGCAGGATGACTCCGAATGCTC
 601 E N H S F K Q N V D R Y A L L S T L Q L 650
 CGAGAACCACAGCTTCAAGCAAAACGTGGACCGTTATGCCTTGCTGTCAACCTTGAGCT
 661 M Y T V G Y S F S L I S L F L A L T L L 720
 GATGTACACCGTGGGATACTCCTTCTCTCTTATCTCCCTCTTCTGGCTCTCACCTCTC
 721 L F L R K L H C T R N Y I H M N L F A S 780
 CTGTTTCTTCGAAAACCTCCACTGCACGGCAACTACATCCACATGAACCTGTTGCTTC
 781 F I L R T L A V L V K D V V F Y N S Y S 840
 TTTTCATCCTGAGAACCTTGGCTGTACTGGTGAAGGACGTCGTCTTCTACAACTCTTACTC
 841 K R P D N E N G W M S Y L S E M S T S C 900
 CAAGAGGCCTGACAATGAGAATGGGTGGATGTCCTACCTGTGAGAGATGTCCACCTCCTG
 901 R S V Q V L L H Y V G A N Y L W L L V 950
 CCGCTCAGTCCAGGTTCTCTTGCACTACTTGTGGGTGCCAATTACTTATGGCTGCTGGT
 961 E G L Y L H T L L E P T V L P E R R L W 1020
 TGAAGGCCTCTACCTCCACACGCTGCTGGAGCCCAAGTGCTTCTGAGAGGCGGCTGTG

FIGURE 6A

09331127 10199

P R Y L L L G W A F P V L F V V P W G F
 1021 G C C C A G A T A C C T G C T G T T G G G G C C T T C C C T G T G C T A T T T G T T G T A C C C T G G G G T T T 1030
 A R A H L E N T G C W T T N G N K K I W
 1081 C G C C C G T G C A C C C T G G A G A A C A C A G G G T G C T G G A C A A C A A T G G G A A T A G A A A T C T G 1140
 W I I R G P M M L C V T V N F F I F L K
 1141 G T G G A T C A T C C G A G G A C C C A T G A T G C T C T G T G T A A C A G T C A A T T T C T T C A T C T T C C T G A A 1200
 I L K L L I S K L K A H Q M C F R D Y K
 1201 A A T T C T C A A G C T T C T A T T T C T A A G C T C A A G C T C A T C A A T G T G C T T C A G A G A T T A T A A 1260
 Y R L A K S T L V L I P L L G V H E I L
 1261 A T A C A G A T T G G C A A A T C A A C A C T G G T C C T C A T T C C T T T A T T G G G C G T T C A T G A G A T C C T 1320
 F S F I T D D Q V E G F A K L I R L F I
 1321 C T T C T C T T T C A T C A C T G A T G A T C A A G T T G A A G G A T T G C A A A C T T A T A C G A C T T T T C A T 1380
 Q L T L S S F H G F L V A L Q Y G F A N
 1381 T C A G T T G A C A C T G A G C T C C T T T C A T G G G T T C C T G G T G G C C T T G C A G T A T G G T T T G C C A A 1440
 G E V K A E L R K Y W V R F L L A R H S
 1441 T G G A G A A G T G A A G G C T G A G C T G C G G A A A T A C T G G G T C C G C T T C T T G C T A G C C C G C C A C T C 1500
 G C R A C V L G K D F R F L G K C P K K
 1501 A G G C T G C A G A G C C T G T G C C T G G G G A A G G A C T T C C G G T T C C T A G G A A A T G T C C C A A G A A 1560
 L S E G D G A E K L R K L Q P S L N S G
 1561 G C T C T C G G A A G G A G A T G G C G T G A G A A G C T T C G G A A G C T G C A G C C C T C A C T T A A C A G T G G 1620
 R L L H L A M R G L G E L G A Q P Q Q D
 1621 G C G G C T C C T A C A T C T A G C C A T G C G A G G T C T T G G G G A G C T G G G C G C C C A G C C C A A C A G G A 1680
 H A R W P R G S S L S E C S E G D V T M
 1681 C C A T G C A C G C T G G C C C C G G G C A G C A G C C T G T C C G A G T G C A G T G A G G G G A T G T C A C C A T 1740
 A N T M E E I L E E S E I
 1741 G G C C A A C A C C A T G G A G G A G A T T C T G G A A G A G A T G A G A T C T A G G G T G G A G T T C C A C C A C C 1800
 C T G G C T C T G C T C C C A G G S A C T C T T G A G S G G G C C C A G G A A G A G G A A G C A A A G C A G G A C A C A
 1801 1860
 C G T T G C T G G G C A C G G A A T C A T T C T C G T T C C A T T C A C C A T G C C A C T T T G A T A T G A A A G C T A
 1861 1920
 T C A C A A G G T T C T T C A A G C T C T G T A T G A A G A G G C T G T G T C A T G C T C A C A G C C T C T G C C
 1921 1980
 T G C T C T T C A T C C T A A T A A C C C C C A C C A G T G T G T T T T C C A C A A T G C C C A C C A G A C C C T A
 1981 2040
 G G G C C T G G C T C T A A A T T C A A G C C A A T G A A G T C C C A C C C G G A A T T C T T T T G C T T T T A C C C
 2041 2100
 C T G G A A G A A A T A
 2101 2112

FIGURE 6B

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Human GLP-2 Receptor Complete Open Reading Frame
Note: Translation may start with M-1 or M-25.
Length: 553 April 21, 1997 07:42 Type: P Check: 2776

1 MXLGSRRAGP GRGSAGLLPG VHELPMGIPA PWGTSPLSFH RXCSLWAPGR
51 PFTLVLLVS IKQVTGSLLS ETTRKWAQYK QACLRDLLKE PSGIFCNGTF
101 DQYVCWPHSS PGNVSVPCPS YLPWWSEESS GRAYRHCLAQ GTWQTIENTAT
151 DIWQDDSECS ENHSFKQNV DRYALLSTLQL MYTVGYSFSL ISLFLALTLL
201 LFLRKLHCTR NYIHNNLFAS FILRTLAVLV KDVVVFYNSYS KRPDNENGWM
251 SYLSEMSTSC RSVQVLLHYF VGANYLWLLV EGLYLHTLLE PTVLPERRLW
301 PRYLLLGWAF PVLFVVPWGF ARAHLENTGC WTTNGNKKIW WIIRGPMMLC
351 VTVNFFIFLK ILKLLISKLK AHQMCFRDYK YRLAKSTLVL IPLLGVHEIL
401 FSFITDDQVE GFAXLIRLFI QLTLSFFHGF LVALQYGFAN GEVXAE LRKY
451 WVRFLARHS GCRACVLGKD FRFLGKCPKK LSEG DGA EKL RKLQPSLNSG
501 RLLHLAMRGL GELGAQPQOD HARWPRGSSL SECSEGDVTM ANTMEEILEE
551 SEI

FIGURE 7

09/331127

666707 227660

cAMP Response to GLP-2

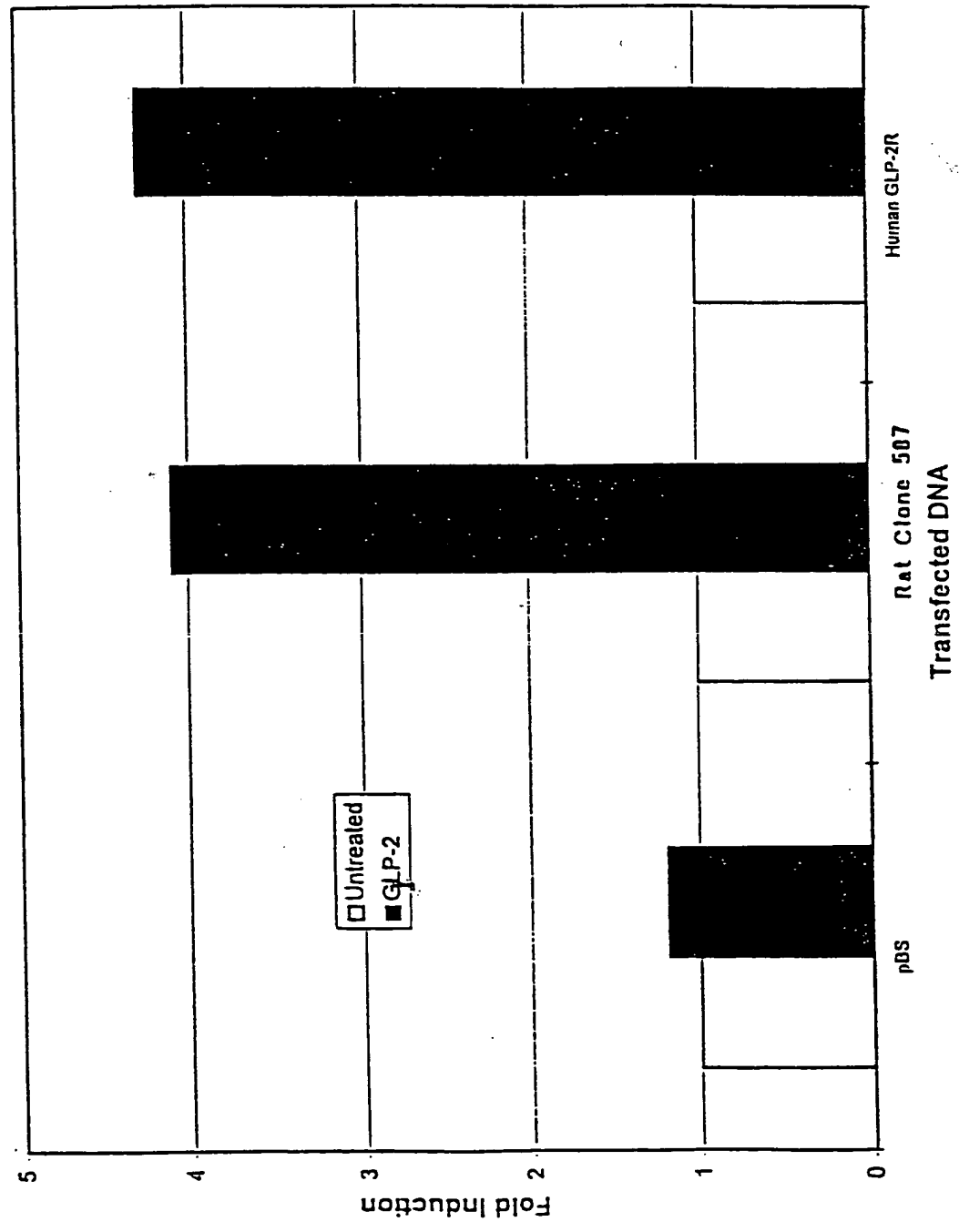


FIGURE 8

1 MRPQPSPAVPSRCREAPVPRVRAQPVGIPEAQGPVPLHSQOMRLLWGPGR 50
 | : | | | | . | | | . | | | | | | | | | |
 1 MKLGSSRAGPGRGSAGLLPGVHELPMGIPAPWGTSPLSFHRKCSLWAPGR 50
 51 PFLALLLLVSIKQVTGSLLKETTQKWANYKEKCLEDLHNRLSGIFCNGTF 100
 | | | | . | | | | | | | | | | . | | | | | | | | | |
 51 PFLTLLVLLVSIKQVTGSLLLEETTRKWAQYKQACLRDLLKEPSGIFCNGTF 100
 101 DRYVCWPHSYPGNVSVPCPSYLPWWNAESPGRAYRHCLAQGTWQTRENTT 150
 | . | | | | | | | | | | | | | | | | | | | | | | | | | |
 101 DQYVCWPHSSPGNVSVPCPSYLPWWSEESSGRAYRHCLAQGTWQTIENAT 150
 151 DIWQDESECSSENHSFRQNVDPHYALLYTLQLMYTVGYSVSLISLFLALTFL 200
 | | | | : | | | | | | | | | | | | | | | | | | | | | |
 151 DIWQDDSECSSENHSFKQNVDRYALLSTLQLMYTVGYSFSLISLFLALTLL 200
 201 LFLRKLHCTRNHYIHMNLFASFILKVLAVLVKDMVSHNSYSKRPDDESGWM 250
 | | | | | | | | | | | | | | : | | | | | | | | | | . | | | |
 201 LFLRKLHCTRNHYIHMNLFASFILRTLAVLVKDVVFYNSYSKRPDNENGWM 250
 251 SYLSETSVSCRSVQVLLHYFVGNTNHLWLLVEGLYLHTLLEPTVFPERRLW 300
 | | | | | | | | | | | | | | : | | | | | | | | | | | | | |
 251 SYLSEMSTSCRSVQVLLHYFVGANYLWLLVEGLYLHTLLEPTVLPERRLW 300
 301 PKYLVVGWAFPMFLFVIPWGFARAHLENTRCWATNGNLKIWWIIRGPMMLC 350
 | : | | . | | | | . | | | : | | | | | | | | | | | | | | : | |
 301 PRYLLLGWAFPVLFVVPWGFARAHLENTGCWTTNGNKKIWWIIRGPMMLC 350
 351 VTVNFFIFLKILKLLISKLLKAHQMCFRDYKYRLAKSTLLLIPLLGVHEVL 400
 | | | | | | | | | | | | | | | | | | | | | | | | | | : | |
 351 VTVNFFIFLKILKLLISKLLKAHQMCFRDYKYRLAKSTLVLIPLLGVHEIL 400
 401 FTFFPDQVQGFSKRIRLFIQTLTSSVHGFLVALQYGFANGEVKAELRKS 450
 | . | | | | : | | . | | | | | | | | | | | | | | | | | | |
 401 FSFITDDQVEGFAKLIRLFIQTLTSSFHGFLVALQYGFANGEVKAELRKY 450
 451 WGRFLLARHWGCRCTCVLGKNFRFLGKCSKLLSEGDSGLTQKLRFTSCSS 500
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 451 WVRFLLARHSGCRACVLGKDFRFLGKCPKLLSEGDAEKLRLQPSLNSG 500
 501 ...HLASETLGDVGVPQPHRGAWPRGSSLSSESSEGDFTLANTMEEILEE 547
 | | | | | | | | : | | | | | | | | | | | | | | | | | | |
 501 RLLHLAMRGLGELGAQPQODHARWPRGSSLSECSEGDVTMANTMEEILEE 550
 548 SEI 550
 | | |
 551 SEI 553

FIGURE 9

12/12

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

MRPQSPAVPSRCREAFVPRVRAQPVGIPEAQGPVPLHSQQMRLLWGPGRPFLALLLLV
MKLGSSRAGPGRGSAGLLPGVHELPMGIPAPWGTSPLSFHRKCSLWAPGRPFLTLVLLV
-----MAGAPGPLRLALLLLGMVGRAGPRP-----
* * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

SIKQVTGSLLKETTQKWANYKEKCLEDLHNRL---SGIFCNGTDFDRYVCWPHSSYPG-NVS
SIKQVTGSLLLEETTRKWAQYKQACLRLDLKEP---SGIFCNGTDFDYVCWPHSSYPG-NVS
---QGATVSLWETVQKWREYRRQCQORSLTEDPPPATDLFCNRTFDEYACWPDGEPGSFVN
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

VPCPSYLPWWNAESPGRAYRHCLAQGTWQTRNTTDIWDQDESECSEHNSFRQNVDRYALL
VPCPSYLPWWSEESSGRAYRHCLAQGTWQTIENATDIWDQDESECSEHNSFKQNVDRYALL
VSCPWYLPWASSVPQGHVYRFCTAEGWLQKDNSSLPWDRDLSECEESKRGERSSPEEQLL
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

YTLQLMYTVGYSVSLISLFLALTLFLFLRKLHCTRNYIHMNLFASFILKVLAVLVKDMVS
STLQLMYTVGYSFSLISLFLALTLFLFLRKLHCTRNYIHMNLFASFILRTLAVLVKDVVF
F-LYIIYTVGYALSFSALVIASAILLGFRHLHCTRNYIHLNLFASFILRALSVMFKDAAL
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

HNSYSKRPDDESGWMSYLS-ETSVSCRSVQVLLHYFVGTHNLWLLVEGLYLHTLLEPTVF
YNSYSKRPDNENGWMSYLS-EMSTSCRSVQVLLHYFVGANYLWLLVEGLYLHTLLEPTVL
KWMYST-AAQQHQWDGLLSYQDSLSCRLVFLMQYCVAANYWLLVEGVLYLTLLAFSVF
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

PERRLWPKYLVVGWAFPMFLVFPWGFARAHLENTRCWATNGNLKIWWIIRGPMMLCVTVN
PERRLWPRYLLLGWAFPVLFVVPWGFARAHLENTGCWTTNGNKKIWWIIRGPMMLCVTVN
SEQWIFRLYVSIWGVPLLFVVPWGVIVKLYEDEGCWTRNSNMNYWLIIRLPILFAIGVN
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

FFIFLKILKLLISKLAHQMCFRDYKYRLAKSTLLIPLLGVHEVLFTFFPDDQVQGFSEK
FFIFLKILKLLISKLAHQMCFRDYKYRLAKSTLVLIPLLGVHEILFSFITDDQVEGFAK
FLIFVRVICIVVSKKANLMCKTDIKCRLAKSTLTLLIPLLGTHEVIFAFVMDEHARGTLR
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

RIRLFIQTLTSSVHGFLVALQYGFANGEVKAELRKSWGRFLLARHWGCRTCVLGKXNFRFL
LIRLFIQTLTSSFHGFVALQYGFANGEVKAELRKYVWRFLARHSGCRACVLGKDFRFL
FIKLFTELSFTSFQGLMVAILYCFVNNEVQLEFRKSWERWRLEHLHIQRDSSMKP-----
* * * * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

GKCSKKLSEGDGSETLQKLRFTSCSS---HLASETLGDVGVPHRGRGAWPRGSSLSSESS
GKCPKKLSEGDGAELKRLQPSLNSGRLLHLAMRGLGELGAQPQDQDARWPRGSSLSSECS
LKCPSTSS-LSSGATAGSSMYTATCQASCS-----
* * *

GL2R_RAT_R
HWBRPAT_TR
GLPR_HUMAN

EGDFTLANTMEEILEESEI
EGDVTMANTMEEILEESEI

FIGURE 10